

Blast Result

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

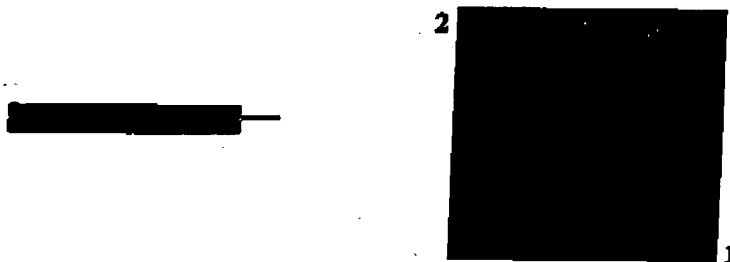
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.9 [May-01-2004]

Match: 1 Mismatch: 2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☐

Sequence 1 lcl|seq_1 Length 6169 (1 .. 6169)

Sequence 2 lcl|seq_2 Length 5271 (1 .. 5271)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1.014e+04 bits (5271), Expect = 0.0
Identities = 5271/5271 (100%)
Strand = Plus / Plus

Query: 1 atctttgttcagtttaoctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60
|||||
Sbjct: 1 atctttgttcagtttacctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60

Query: 61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120
|||||
Sbjct: 61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120

Query: 121 ggaagaaggagtatccacgtagccaagtgtccaggctgtgtctgtcttatttttagtga 180
|||||
Sbjct: 121 ggaagaaggagtatccacgtagccaagtgtccaggctgtgtctgtcttatttttagtga 180

Query: 181 cagatgttgctcctgcagagaagctattcttcaggaaacatcacatccaatatggtaaatac 240
|||||
Sbjct: 181 cagatgttgctcctgcagagaagctattcttcaggaaacatcacatccaatatggtaaatac 240

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Query: 241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300
|||||
Sbjct: 241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300

Query: 301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360
|||||
Sbjct: 301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360

Query: 361 atgaggaccaaaatcaatgaataaggaaaaacagctcagaaaaagatgtttccaaattgg 420
|||||
Sbjct: 361 atgaggaccaaaatcaatgaataaggaaaaacagctcagaaaaagatgtttccaaattgg 420

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Sbjct: 421 taattaagtatttgttccttgggaagagacctccatgtgagcttgatgggaaaaatgggaa 480

Query: 481 aaacgtcaaaagcatgatctgatcagatcccaaagtggtattatttttaaaaaccagat 540
|||||
Sbjct: 481 aaacgtcaaaagcatgatctgatcagatcccaaagtggtattatttttaaaaaccagat 540

Query: 541 ggcatacactctggggaggcaagttcaggaaggtcatgttagcaaaggacataacaataac 600
|||||
Sbjct: 541 ggcatacactctggggaggcaagttcaggaaggtcatgttagcaaaggacataacaataac 600

Query: 601 agcaaaatcaaaattccgcaaatgcaggaggaaaaatggggactgggaaagctttcataac 660
|||||
Sbjct: 601 agcaaaatcaaaattccgcaaatgcaggaggaaaaatggggactgggaaagctttcataac 660

Query: 661 agtgattaggcagttgaccatgttcgcaacacctcccgtctataccagggaacacaaaa 720
|||||
Sbjct: 661 agtgattaggcagttgaccatgttcgcaacacctcccgtctataccagggaacacaaaa 720

Query: 721 attgactgggctaagcctggactttcaagggaatatgaaaaactgagagcaaaacaaaa 780
|||||
Sbjct: 721 attgactgggctaagcctggactttcaagggaatatgaaaaactgagagcaaaacaaaa 780

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Sbjct: 781 gacatgggttaaaaggcaaccagaacattgtgagccttcaaagcagcagtgcccotcagca 840

Query: 841 gggaccctgaggcatttgccttttaggaaggccagttttcttaaggaatcttaagaaactc 900
|||||
Sbjct: 841 gggaccctgaggcatttgccttttaggaaggccagttttcttaaggaatcttaagaaactc 900

Query: 901 ttgaaagatcatgaattttaaccattttaagtataaaacaaatatgcgatgcataatcag 960
|||||
Sbjct: 901 ttgaaagatcatgaattttaaccattttaagtataaaacaaatatgcgatgcataatcag 960

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Query: 961 tttagacatgggtcccaattttataaagtcaggcatacaaggataacgtgtcccagctcc 1020
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Sbjct: 961 tttagacatgggtcccaattttataaagtcaggcatacaaggataacgtgtcccagctcc 1020

Query: 1021 ggataggtcagaaatcattagaaatcactgtgtccccatcctaactttttcagaatgatc 1080
|||||
Sbjct: 1021 ggataggtcagaaatcattagaaatcactgtgtccccatcctaactttttcagaatgatc 1080

Query: 1081 tgtcatagccctcacacacaggcccgatgtgtctgacctacaaccacatctacaacccaa 1140
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Sbjct: 1081 tgtcatagccctcacacacaggcccgatgtgtctgacctacaaccacatctacaacccaa 1140

Query: 1141 gtgcctcaaccattgttaacgtgtcatctcagtaggtcccattacaaatgccacctcccc 1200
|||||
Sbjct: 1141 gtgcctcaaccattgttaacgtgtcatctcagtaggtcccattacaaatgccacctcccc 1200

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Sbjct: 1201 tgtgcagcccatcccgctccacaggaagtctcccaactctagactttctgcatcacgatgt 1260

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Sbjct: 1261 tacagccagaagctccgtgaggggtgagggctgtgtcttacacctacctgtatgctctac 1320

Query: 1321 acctgagctcactgcaacctctgcctcccagggttcaagcaattctcctgtctcagcctcc 1380
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Sbjct: 1321 acctgagctcactgcaacctctgcctcccagggttcaagcaattctcctgtctcagcctcc 1380

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Sbjct: 1381 cgggtagctgggactacaggcgacgcccggctaattttgtattgttagtagagatggg 1440

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Sbjct: 1441 gtttcaccatattagcccggtggtcttgaactcctgacctcaggtgatccaccacctc 1500

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Sbjct: 1501 agcctcctaaagtgtctgggattacaggcatgagtcaccgcgcccgccaagggtcagtg 1560

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Sbjct: 1561 ttaataaggaataacttgaatggtttactaaaccaacagggaacagacaaaagctgtga 1620

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Sbjct: 1621 taatttcagggattcttgggatggggaatggtgccatgagctgcctgcctagtccagac 1680

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Query: 1681 cactggtoctcatcactttcttccctcatcctcattttcaggctaagttaccattttatt 1740
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Sbjct: 1681 cactggtoctcatcactttcttccctcatcctcattttcaggctaagttaccattttatt 1740

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Sbjct: 1741 caccatgcttttgtggtaagcctccacatcggttactgaaataagagtatacataaactag 1800

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Sbjct: 1801 ttccatttggggccatctgtgtgtgtgtatagggaggagggcataccccagagactcct 1860

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Sbjct: 1921 tgggtgtcctgagcaacctgccagcccggtccactggttgttttgttatcactctctagg 1980

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Sbjct: 2341 gectcgcttcccgatgaatcgtoctggtgcatctgagctggagactccttgggtccaggct 2400

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Query: 2401 ccagaaaggaaatggagagggaaactagtctaacggagaatctggaggggacagtgtttc 2460
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Sbjct: 2521 tggggacgctggggctgagcgggtgctgaaaggcaggaaggtgaaaagggcaaggctgaa 2580

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Sbjct: 3001 ataaagacccttgagctctcgtgttctgtgaacacttcctgtgattctctgtgagggg 3060

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Sbjct: 3061 ggatgttgagaggggaaggaggcagagctggagcagctgagccacaggggaggtggaggg 3120

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Sbjct: 3121 ggacaggaaggcaggcagaagctgggtgctccatcagtcctcactgatcacgtcagactc 3180

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Sbjct: 3181 caggaccgagagccacaatgcttcaggaaagctcaatgaacccaacagccacattttcct 3240

Query: 3241 tccctaagcatagacaatggcatttgccaataacccaaaagaatgcagagactaactggt 3300
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Sbjct: 3241 tccctaagcatagacaatggcatttgccaataacccaaaagaatgcagagactaactggt 3300

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Sbjct: 3301 ggtagcttttgctggcattcaaaaactgggccagagcaagtggaaaatgccagagattg 3360

Query: 3361 ttaaacttttcaccctgaccagcacccacgcagctcagcagtgactgctgacagcacgg 3420
|||||
Sbjct: 3361 ttaaacttttcaccctgaccagcacccacgcagctcagcagtgactgctgacagcacgg 3420

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Query: 3601 cctgattttotaataactatatttttcttttacaagctgagtaattctgagcaagtcacaag 3660
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Sbjct: 3661 gtagtaactgaggctgtaagattacttagtttctccttattaggaactctttttctctgt 3720

Query: 3721 ggagttagcagcacaaagggcaatcccgtttcttttaacaggaagaaaacattcctaagag 3780
|||||
Sbjct: 3721 ggagttagcagcacaaagggcaatcccgtttcttttaacaggaagaaaacattcctaagag 3780

Query: 3781 taaagccaaacagattcaagcctaggtcttgctgactatatgattgggtttttgaaaaat 3840
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Sbjct: 3781 taaagccaaacagattcaagcctaggtcttgctgactatatgattgggtttttgaaaaat 3840

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Query: 3841 catttcagcgatgtttactatctgattcagaaaatgagactagtaccottttggtcagctg 3900
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Sbjct: 3841 catttcagcgatgtttactatctgattoagaaaatgagactagtaccottttggtcagctg 3900

Query: 3901 taaacaaacacccagttgtaaatgtctcaagttcaggcttaactgcagaaccaatcaaaa 3960
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Sbjct: 3901 taaacaaacacccagttgtaaatgtctcaagttcaggcttaactgcagaaccaatcaaaa 3960

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|||||
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Query: 4441 ctttgaaattagacctcctgctggatcttgtttttaacatattaataaaaacatgtttaaa 4500
|||||
Sbjct: 4441 ctttgaaattagacctcctgctggatcttgtttttaacatattaataaaaacatgtttaaa 4500

Query: 4501 attttgatattttgataatcatatttcattatcatttgtttcctttgtaatctatatattt 4560
|||||
Sbjct: 4501 attttgatattttgataatcatatttcattatcatttgtttcctttgtaatctatatattt 4560

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```
CPU time:      0.05 user secs.      0.00 sys. secs      0.05 total secs.
```


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Lambda	K	H
1.33	0.621	1.12

Gapped Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 1926
Number of extensions: 71
Number of successful extensions: 18
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 6169
Length of database: 11,738,793,097
Length adjustment: 27
Effective length of query: 6142
Effective length of database: 11,738,793,070
Effective search space: 72099667035940
Effective search space used: 72099667035940
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (25.0 bits)
S2: 22 (43.0 bits)